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### Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

### SZABO-SCANDIC HandelsgmbH

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## GSTM4 Pre-design Chimera RNAi

Catalog # : H00002948-R01 規格 : [ 10 nmol ] [ 20 nmol ]

List All

### Specification

**Product Description:** Homo sapiens glutathione S-transferase M4 (GSTM4), transcript variant 1, mRNA.

### Application Image

RNAi Knockdown

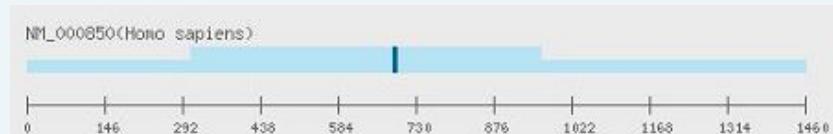
**Reactivity:** Human

**Supplied Product:** DEPC water

**Target Refseq:** NM\_000850

**Storage Instruction:** Store at -20°C, do not exceed 4 - 5 freeze-thaw cycles to ensure product integrity.

**Note:** Position of the Chimera RNAi.



### Publication Reference

1. dsCheck: highly sensitive off-target search software for double-stranded RNA-mediated RNA interference.  
Naito Y, Yamada T, Matsumiya T, Ui-Tei K, Saigo K, Morishita S. Nucleic Acids Res. 2005 Jul 1;33(Web Server issue):W589-91.
2. Functional dissection of siRNA sequence by systematic DNA substitution: modified siRNA with a DNA seed arm is a powerful tool for mammalian gene silencing with significantly reduced off-target effect.  
Ui-Tei K, Naito Y, Zenno S, Nishi K, Yamato K, Takahashi F, Juni A, Saigo K. Nucleic Acids Res. 2008 Apr;36(7):2136-51. Epub 2008 Feb 11.
3. Guidelines for the selection of highly effective siRNA sequences for mammalian and chick RNA interference.  
Ui-Tei K, Naito Y, Takahashi F, Haraguchi T, Ohki-Hamazaki H, Juni A, Ueda R, Saigo K. Nucleic Acids Res. 2004 Feb 9;32(3):936-48. Print 2004.
4. siDirect: highly effective, target-specific siRNA design software for mammalian RNA interference.  
Naito Y, Yamada T, Ui-Tei K, Morishita S, Saigo K. Nucleic Acids Res. 2004 Jul 1;32(Web Server issue):W124-9.

### Applications

#### RNAi Knockdown

#### Gene Information

**Entrez GeneID:** 2948

**Gene Name:** GSTM4

**Gene Alias:** GSTM4-4, GTM4, MGC131945, MGC9247

**Gene** glutathione S-transferase mu 4

**Description:**

**Omim ID:** [138333](#)

**Gene Ontology:** [Hyperlink](#)

**Gene Summary:** Cytosolic and membrane-bound forms of glutathione S-transferase are encoded by two distinct supergene families. At present, eight distinct classes of the soluble cytoplasmic mammalian glutathione S-transferases have been identified: alpha, kappa, mu, omega, pi, sigma, theta and zeta. This gene encodes a glutathione S-transferase that belongs to the mu class. The mu class of enzymes functions in the detoxification of electrophilic compounds, including carcinogens, therapeutic drugs, environmental toxins and products of oxidative stress, by conjugation with glutathione. The genes encoding the mu class of enzymes are organized in a gene cluster on chromosome 1p13.3 and are known to be highly polymorphic. These genetic variations can change an individual's susceptibility to carcinogens and toxins as well as affect the toxicity and efficacy of certain drugs. Diversification of these genes has occurred in regions encoding substrate-binding domains, as well as in tissue expression patterns, to accommodate an increasing number of foreign compounds. Multiple transcript variants, each encoding a distinct protein isoform, have been identified. [provided by RefSeq]

**Other** GST class-mu 4,GTS-

**Designations:** Mu2,OTTHUMP00000013356,OTTHUMP00000013358,S-(hydroxyalkyl)glutathione lyase M4,glutathione S-alkyltransferase M4,glutathione S-aralkyltransferase M4,glutathione S-aryltransferase M4,glutathione S-transferase M4

## Gene Pathway

[Drug metabolism - cytochrome P450 Glutathione metabolism](#)

[Metabolism of xenobiotics by cytochrome P450](#)

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